EFFECTS OF THREE DIFFERENT ALLELES AT THE RN LOCUS ON COLOUR CHARACTERISTICS OF PORK LOIN FROM A HAMPSHIRE X LANDRACE CROSS

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Background

Milan et al. (2000) found that the dominat RN^- mutation in Hampshire pigs, which causes high glycogen content in skeletal muscle, is a nonconservative substitution (R200Q) in the PRKAG3 gene. It is known that the RN^- gene influences the colour of pork (Lundström et al., 1996; Hamilton et al., 2000; Le Roy et al., 2000). Recently the presence of a new allele (V199I) in the PRKAG3 gene that affects the glycogen content and certain meat quality traits, such as ultimate pH and colour, has been found in the pig breeds Landrace, Large White, Berkshire, Duroc and Duroc Synthetic (Ciobanu et al., 2001). This new allele (V199I) has now been identified in a Swedish pig material of a Hampshire x Landrace cross, and its effect on the colour of pork loin has been studied.

Objectives

The aim of this study was to get knowledge of the effects of the three different alleles RN^-, rn^+ and V199I (here called rn*) at the RN locus in the PRKAG3 gene on the colour of pork loin from a Hampshire x Landrace cross.

Methods

M. longissimus dorsi from the animal material described by Enfält et al. (2002) was used for colour, pH (Knick Portamess 651, Xerolyt electrode, W. Ingold Ltd, Urdorf, Switzerland) and fibre optic probe (FOP, 900 nm; TBL Fibre Optic Groups, Leeds, UK) measurements. The colour was measured 3 days after slaughter (after 1.5-2h blooming at 4°C) on a 2 cm slice cut at the last rib. A Hunterlab Color Quest Instrument (Hunter Associates Laboratory, Inc., Reston, VA 22090 USA), specular reflectance excluded, 25 mm aperture, illuminant D65, 10° Standard Observer and CIE (1976) colour scale was used. The relative contents of Mb, MbO and MetMb were calculated from the reflectance curve according to Krzywicki (1979) using 710 nm instead of 730 nm. Reflectance values at wavelengths not given by the instrument (473, 525 and 572 nm) were calculated using linear interpolation. The pigment content was analysed in part of the material according to Hornsey (1956). The alleles within the PRKAG3 gene were determined according to Milan et al. (2000). Statistical evaluation was performed using the Mixed Procedure in SAS (Ver. 8e, SAS Institute Inc., Cary, NC, USA). The model contained the effects of genotype, breed cross, sex and time of slaughter (see Enfält et al., 2002). Carcass weight was included in the model when significant.

Results and Discussion

Six different RN genotypes were identified in the present material (Table 1). The recently identified rn* allele was found in combination with both the RN^- and the rn^+ allele. Furthermore, a low frequency of the rn*/rn* genotype was present. The pH drop was slightly faster for the RN^- genotypes compared with the rn^+ and rn* genotypes. pH_u was highest in the rn* genotypes, lowest in the RN^- genotypes and in between in the rn^+/rn^+ genotype. The slightly faster pH drop in the RN^- genotypes did not influence the internal reflectance, as no significant differences between the genotypes in FOP values were found. There was a tendency to higher pigment content in the RN^-/RN^- genotype compared with the rn* genotypes.

Table 1. Least squares means (LSM) of pH and FOP at different times after slaughter and pigment content (hemin)

	Genotype					
Quality parameter	RN^-/RN^-	RN^-/rn^+	RN^-/rn^*	rn^+/rn^+	rn^+/rn^*	rn*/rn*
n	78	80	111	27	29	7
pH_{3h}	6.11a[1]	6.03b (n=78)	6.08ab	6.23c	6.26c	6.16abc
pH_{24h}	5.44a	5.42b	5.43ab	5.46c	5.51d	5.52d
pH_u (48h)	5.33a (n=83)	5.33a (n=83)	5.33a (n=114)	5.36b	5.42c	5.42c (n=10)
FOP_{24h}	26	26	27	26	25	27
FOP_{72h}	35 (n=43)	35 (n=62)	36 (n=64)	30 (n=19)	30 (n=23)	31 (n=8)
Hemin (mg/kg)	39.7 (n=18)	36.2 (n=25)	35.7 (n=16)	37.5 (n=17)	35.4 (n=18)	34.1 (n=4)

[1] Significant differences between LSM with different letters within the same row, $p \leq 0.05$

The pork colour was influenced by the different alleles at the RN locus (Fig. 1). The RN^- allele gave significantly higher a* and b* values compared with the rn^+ and rn* alleles. There were only small or no differences between the RN^- genotypes in L*, a* and b* values as well as in the myoglobin forms. The rn^+/rn^* genotype showed the most marked effect on the colour characteristics, lowest L*, a* and b* values, lowest fraction of MbO and MetMb and highest fraction of Mb. The rn*/rn* genotype showed the same tendency on the colour characteristics, however with less marked effects. The colour of meat depends on many factors such as pigment content, myoglobin form and physical characteristics of the meat affecting the internal reflectance (Lindahl et al., 2001). The colour differences between genotypes with the RN^- allele and the rn^+/rn^* genotype may be explained by the differences in the myoglobin forms, as only small differences in internal reflectance and pigment content were found. Low fractions of MbO and high fractions of Mb result in darker and less red and less yellow pork colour (Lindahl et al., 2001). In agreement with the present study, Le Roy et al. (2000) found higher a* and b* values in RN^- gene carriers compared with non-carriers, but also higher L* values. Hamilton et al. (2000) found higher L* and b* values, but no significant difference in a* value in RN^- gene carriers compared with non-carriers in Hampshire pigs.

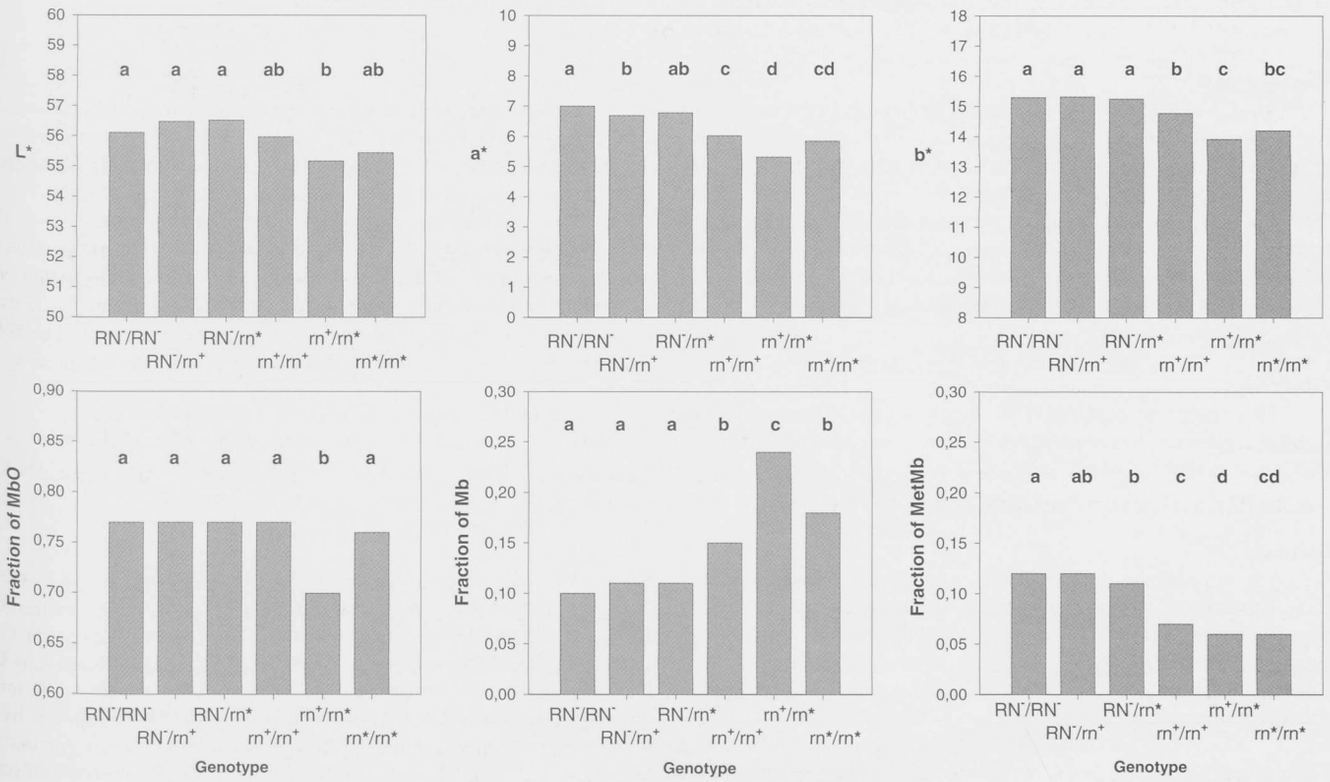

Figure 1. Lightness (L*), redness (a*), yellowness (b*) and fractions of the myoglobin forms oxymyoglobin (MbO), deoxymyoglobin (Mb) and metmyoglobin (MetMb). Significant differences between LSM with different letters within the same diagram, $p \leq 0.05$.

Conclusions

All the three alleles at the RN locus affected the colour of pork loin. The RN^- allele was dominant, giving more red (high a*) and more yellow (high b*) colour. The rn* allele tended to be dominant over the rn^+ allele, giving the darkest (low L*), less red (low a*) and less yellow (low b*) colour. The colour differences were mainly explained by differences in the myoglobin forms.

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Pertinent literature

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